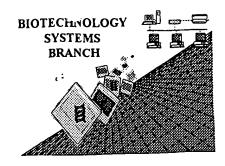# RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: _09/674,379_

Source: _PCT/09_

Date Processed by STIC: _4/25/2001_

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY
FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)
PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.
Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO).
Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:
http://www.uspto.gov/web/offices/pac/checker

Raw Sequence Listing Error Summary

<u>ERROR DETECTED</u> <u>SUGGESTED CORRECTION</u>   SERIAL NUMBER: _09/674,379_

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 _____ Wrapped Nucleics   The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".

2 _____ Wrapped Aminos   The amino acid number/text at the end of each line "wrapped " down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".

3 _____ Incorrect Line Length   The rules require that a line not exceed 72 characters in length. This includes spaces.

4 _____ Misaligned Amino Acid Numbering   The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and use spacing between the numbers.

5 _____ Non-ASCII   This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.

6 _____ Variable Length   Sequence(s) _____ contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and
indicate in the (ix) feature section that some may be missing.

7 _____ PatentIn ver. 2.0 "bug"   A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. **This applies primarily to the mandatory <220>-<223> sections for Artificial or Unknown sequences.**

8 _____ Skipped Sequences (OLD RULES)   Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X:
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).

9 _____ Skipped Sequences (NEW RULES)   Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence.
<210> sequence id number
<400> sequence id number
000

10 _____ Use of n's or Xaa's (NEW RULES)   Use of n's and/or Xaa's have been detected in the Sequence Listing.
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

11 _____ Use of "Artificial" (NEW RULES)   Use of "Artificial" only as "<213> Organism" response is incomplete, per 1.823(b) of New Sequence Rules.
Valid response is Artificial Sequence.

12 _____ Use of <220>Feature (NEW RULES)   Sequence(s) _____ are missing the <220>Feature and associated headings.
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial Sequence" or "Unknown"
Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32)   (Sec. 1.823 of new Rules)

13 _____ PatentIn ver. 2.0 "bug"   **Please do not use "Copy to Disk" function of PatentIn version 2.0.** This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).
Instead, please use "File Manager" or any other means to copy file to floppy disk.

AMC - Biotechnology Systems Branch - 4/06/2001

PCT

Does Not Comply
Corrected Diskette Needed
see pp. 4, 6

```
 3 <110> APPLICANT: Ono Pharmaceutical Co., Ltd.
 5 <120> TITLE OF INVENTION: A novel polypeptide, a cDNA encoding the polypeptide
 6       and utilization thereof
 8 <130> FILE REFERENCE: Q61531
10 <140> CURRENT APPLICATION NUMBER: US/09/674,379
11 <141> CURRENT FILING DATE: 2000-10-30
13 <150> PRIOR APPLICATION NUMBER: PCT/JP99/02284
14 <151> PRIOR FILING DATE: 1999-04-28
16 <150> PRIOR APPLICATION NUMBER: JP HEI 10-119731
17 <151> PRIOR FILING DATE: 1998-04-28
19 <160> NUMBER OF SEQ ID NOS: 17
21 <170> SOFTWARE: PatentIn Ver. 2.1
23 <210> SEQ ID NO: 1
24 <211> LENGTH: 1344
25 <212> TYPE: DNA
26 <213> ORGANISM: Mus musculus
28 <400> SEQUENCE: 1
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30 gggaatgcac agcagcagtg cacaaacggc tttgacctgg accgccagtc aggacagtgt 120
31 ctagatattg atgaatgccg gaccatccct gaggcttgtc gtggggacat gatgtgtgtc 180
32 aaccagaatg gcgggtattt gtgcatccct cgaaccaacc cagtgtatcg agggccttac 240
33 tcaaatccct actctacatc ctactcaggc ccatacccag cagcggcccc accagtacca 300
34 gcttccaact accccacgat ttcaaggcct cttgtctgcc gctttgggta tcagatggat 360
35 gaaggcaacc agtgtgtgga tgtggacgag tgtgcaacag actcacacca gtgcaaccct 420
36 acccagatct gtatcaacac tgaaggaggt tacacctgct cctgcaccga tgggtactgg 480
37 cttctggaag ggcagtgcct agatattgat gaatgtcgct atggttactg ccagcagctc 540
38 tgtgcaaatg ttccaggatc ctattcctgt acatgcaacc ctggtttcac cctcaacgac 600
39 gatggaaggt cttgccaaga tgtgaacgag tgcgaaactg agaatccctg tgttcagacc 660
40 tgtgtcaaca cctatggctc tttcatctgc cgctgtgacc aggatatga acttgaggaa 720
41 gatggcattc actgcagtga tatggacgag tgcagcttct ccgagttcct ctgtcaacac 780
42 gagtgtgtga accagccggg ctcatacttc tgctcgtgcc ctccaggcta cgtcctgttg 840
43 gatgataacc gaagctgcca ggatatcaat gaatgtgagc accgaaacca cacgtgtacc 900
44 tcactgcaga cttgctacaa tctacaaggg ggcttcaaat gtattgatcc catcagctgt 960
45 gaggagcctt atctgctgat tggtgaaaac cgctgtatgt gtcctgctga gcacaccagc 1020
46 tgcagagacc agccattcac catcctgtat cgggacatgg atgtggtgtc aggacgctcc 1080
47 gttcctgctg acatcttcca gatgcaagca acaacccgat accctggtgc ctattacatt 1140
48 ttccagatca aatctggcaa cgagggtcga gagttctata tgcggcaaac agggcctatc 1200
49 agtgccaccc tggtgatgac acgccccatc aaagggcctc gggacatcca gctggacttg 1260
50 gagatgatca ctgtcaacac tgtcatcaac ttcagaggca gctccgtgat ccgactgcgg 1320
51 atatatgtgt cgcagtatcc gttc                                     1344
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55 <211> LENGTH: 2233
56 <212> TYPE: DNA
57 <213> ORGANISM: Mus musculus
59 <220> FEATURE:
60 <223> OTHER INFORMATION: Clone mouse A55 derived from Day 13 mouse
61       embryonic heart
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RAW SEQUENCE LISTING   DATE: 04/25/2001
PATENT APPLICATION: US/09/674,379   TIME: 07:41:15

Input Set : A:\es.txt
Output Set: N:\CRF3\04252001\I674379.raw

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65 <222> LOCATION: (75)..(1418)
67 <220> FEATURE:
68 <221> NAME/KEY: sig_peptide
69 <222> LOCATION: (75)..(143)
71 <220> FEATURE:
72 <221> NAME/KEY: mat_peptide
73 <222> LOCATION: (144)..(1418)
75 <400> SEQUENCE: 2
76 aattcggcac gagccccagt cccaccgcag agcctgcctt cctcgcgtcg cttctcctcc 60
78 cgcgcatctt ggat atg cca gga tta aaa agg ata ctc act gtt acc atc   110
79               Met Pro Gly Leu Lys Arg Ile Leu Thr Val Thr Ile
80                         -20             -15
82 ttg gca ctc tgg ctt cca cat cct ggg aat gca cag cag cag tgc aca   158
83 Leu Ala Leu Trp Leu Pro His Pro Gly Asn Ala Gln Gln Gln Cys Thr
84    -10               -5              -1  1                   5
86 aac ggc ttt gac ctg gac cgc cag tca gga cag tgt cta gat att gat   206
87 Asn Gly Phe Asp Leu Asp Arg Gln Ser Gly Gln Cys Leu Asp Ile Asp
88                10               15                  20
90 gaa tgc cgg acc atc cct gag gct tgt cgt ggg gac atg atg tgt gtc   254
91 Glu Cys Arg Thr Ile Pro Glu Ala Cys Arg Gly Asp Met Met Cys Val
92              25               30               35
94 aac cag aat ggc ggg tat ttg tgc atc cct cga acc aac cca gtg tat   302
95 Asn Gln Asn Gly Gly Tyr Leu Cys Ile Pro Arg Thr Asn Pro Val Tyr
96          40               45               50
98 cga ggg cct tac tca aat ccc tac tct aca tcc tac tca ggc cca tac   350
99 Arg Gly Pro Tyr Ser Asn Pro Tyr Ser Thr Ser Tyr Ser Gly Pro Tyr
100      55               60                   65
102 cca gca gcg gcc cca cca gta cca gct tcc aac tac ccc acg att tca   398
103 Pro Ala Ala Ala Pro Pro Val Pro Ala Ser Asn Tyr Pro Thr Ile Ser
104  70                75               80                   85
106 agg cct ctt gtc tgc cgc ttt ggg tat cag atg gat gaa ggc aac cag   446
107 Arg Pro Leu Val Cys Arg Phe Gly Tyr Gln Met Asp Glu Gly Asn Gln
108              90               95               100
110 tgt gtg gat gtg gac gag tgt gca aca gac tca cac cag tgc aac cct   494
111 Cys Val Asp Val Asp Glu Cys Ala Thr Asp Ser His Gln Cys Asn Pro
112              105              110              115
114 acc cag atc tgt atc aac act gaa gga ggt tac acc tgc tcc tgc acc   542
115 Thr Gln Ile Cys Ile Asn Thr Glu Gly Gly Tyr Thr Cys Ser Cys Thr
116          120              125              130
118 gat ggg tac tgg ctt ctg gaa ggg cag tgc cta gat att gat gaa tgt   590
119 Asp Gly Tyr Trp Leu Leu Glu Gly Gln Cys Leu Asp Ile Asp Glu Cys
120      135              140              145
122 cgc tat ggt tac tgc cag cag ctc tgt gca aat gtt cca gga tcc tat   638
123 Arg Tyr Gly Tyr Cys Gln Gln Leu Cys Ala Asn Val Pro Gly Ser Tyr
124 150              155              160              165
126 tcc tgt aca tgc aac cct ggt ttc acc ctc aac gac gat gga agg tct   686
127 Ser Cys Thr Cys Asn Pro Gly Phe Thr Leu Asn Asp Asp Gly Arg Ser
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RAW SEQUENCE LISTING   DATE: 04/25/2001
PATENT APPLICATION: US/09/674,379   TIME: 07:41:15

Input Set : A:\es.txt
Output Set: N:\CRF3\04252001\I674379.raw

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128                170            175               180
130 tgc caa gat gtg aac gag tgc gaa act gag aat ccc tgt gtt cag acc    734
131 Cys Gln Asp Val Asn Glu Cys Glu Thr Glu Asn Pro Cys Val Gln Thr
132                185            190             195
134 tgt gtc aac acc tat ggc tct ttc atc tgc cgc tgt gac cca gga tat    782
135 Cys Val Asn Thr Tyr Gly Ser Phe Ile Cys Arg Cys Asp Pro Gly Tyr
136            200              205            210
138 gaa ctt gag gaa gat ggc att cac tgc agt gat atg gac gag tgc agc    830
139 Glu Leu Glu Glu Asp Gly Ile His Cys Ser Asp Met Asp Glu Cys Ser
140     215              220             225
142 ttc tcc gag ttc ctc tgt caa cac gag tgt gtg aac cag ccg ggc tca    878
143 Phe Ser Glu Phe Leu Cys Gln His Glu Cys Val Asn Gln Pro Gly Ser
144 230                235            240             245
146 tac ttc tgc tcg tgc cct cca ggc tac gtc ctg ttg gat gat aac cga    926
147 Tyr Phe Cys Ser Cys Pro Pro Gly Tyr Val Leu Leu Asp Asp Asn Arg
148                250            255            260
150 agc tgc cag gat atc aat gaa tgt gag cac cga aac cac acg tgt acc    974
151 Ser Cys Gln Asp Ile Asn Glu Cys Glu His Arg Asn His Thr Cys Thr
152                265            270            275
154 tca ctg cag act tgc tac aat cta caa ggg ggc ttc aaa tgt att gat    1022
155 Ser Leu Gln Thr Cys Tyr Asn Leu Gln Gly Gly Phe Lys Cys Ile Asp
156        280            285             290
158 ccc atc agc tgt gag gag cct tat ctg ctg att ggt gaa aac cgc tgt    1070
159 Pro Ile Ser Cys Glu Glu Pro Tyr Leu Leu Ile Gly Glu Asn Arg Cys
160     295              300             305
162 atg tgt cct gct gag cac acc agc tgc aga gac cag cca ttc acc atc    1118
163 Met Cys Pro Ala Glu His Thr Ser Cys Arg Asp Gln Pro Phe Thr Ile
164 310            315            320                325
166 ctg tat cgg gac atg gat gtg gtg tca gga cgc tcc gtt cct gct gac    1166
167 Leu Tyr Arg Asp Met Asp Val Val Ser Gly Arg Ser Val Pro Ala Asp
168                330            335            340
170 atc ttc cag atg caa gca aca acc cga tac cct ggt gcc tat tac att    1214
171 Ile Phe Gln Met Gln Ala Thr Thr Arg Tyr Pro Gly Ala Tyr Tyr Ile
172                345            350            355
174 ttc cag atc aaa tct ggc aac gag ggt cga gag ttc tat atg cgg caa    1262
175 Phe Gln Ile Lys Ser Gly Asn Glu Gly Arg Glu Phe Tyr Met Arg Gln
176            360            365            370
178 aca ggg cct atc agt gcc acc ctg gtg atg aca cgc ccc atc aaa ggg    1310
179 Thr Gly Pro Ile Ser Ala Thr Leu Val Met Thr Arg Pro Ile Lys Gly
180     375              380            385
182 cct cgg gac atc cag ctg gac ttg gag atg atc act gtc aac act gtc    1358
183 Pro Arg Asp Ile Gln Leu Asp Leu Glu Met Ile Thr Val Asn Thr Val
184 390                395            400                405
186 atc aac ttc aga ggc agc tcc gtg atc cga ctg cgg ata tat gtg tcg    1406
187 Ile Asn Phe Arg Gly Ser Ser Val Ile Arg Leu Arg Ile Tyr Val Ser
188            410            415            420
190 cag tat ccg ttc tgagcctctg gctaaggcct ctgacactgc ctttcaccag    1458
191 Gln Tyr Pro Phe
192            425
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194 caccgaggga cgggaggaga aaggaaacca gcaagaatga gagcgagaca gacattgcac 1518
196 cttcctgct gaatatctcc tgggggcatc agcctagcat cttgacccat atctgtacta 1578
198 ttgcagatgg tcactctgaa ggacaccctg ccctcagttc ctatgatgca gttatccaaa 1638
200 agtgttcatc ttagcccctg atatgaggtt gccagtgact cttcaaagcc ttccatttat 1698
202 ttccatcgtt ttataaaaaa gaaaatagat tagatttgct ggggtatgag tcctcgaagg 1758
204 ttcaaaagac tgagtggctt gctctcacct cttcctctcc ttcctccatc tcttgctgca 1818
206 ttgctgcttt gcaaagtcc tcatgggctc gtgggaaatg ctgggaatag ctagtttgct 1878
208 tcttgcatgt tctgagaagg ctatgggaac acaccacagc aggatcgaag gtttttatag 1938
210 agtctatttt aaaatcacat ctggtatttt cagcataaaa gaaattttag ttgtctttaa 1998
212 aatttgtatg agtgtttaac cttttcttat tcattttgag gcttcttaaa gtggtagaat 2058
214 tccttccaaa ggcctcagat acatgttatg ttcagtcttt cgaacctcat cctttcctgc 2118
W--> 216 atcttagccc agttttacg aagacccctt aatcatgctt tmttaagagt ttttacccaa 2178
218 ctgcgttgga agacagaggt atccagactg attaaataat tgaagaaaaa aaaaa    2233
221 <210> SEQ ID NO: 3
222 <211> LENGTH: 448
223 <212> TYPE: PRT
224 <213> ORGANISM: Mus musculus
225 <223> OTHER INFORMATION: Clone mouse A55 derived from Day 13 mouse
228 <400> SEQUENCE: 3
229 Met Pro Gly Leu Lys Arg Ile Leu Thr Val Thr Ile Leu Ala Leu Trp
230             -20             -15             -10
232 Leu Pro His Pro Gly Asn Ala Gln Gln Gln Cys Thr Asn Gly Phe Asp
233          -5              -1   1            5
235 Leu Asp Arg Gln Ser Gly Gln Cys Leu Asp Ile Asp Glu Cys Arg Thr
236 10                15              20                 25
238 Ile Pro Glu Ala Cys Arg Gly Asp Met Met Cys Val Asn Gln Asn Gly
239                30               35                 40
241 Gly Tyr Leu Cys Ile Pro Arg Thr Asn Pro Val Tyr Arg Gly Pro Tyr
242             45              50                 55
244 Ser Asn Pro Tyr Ser Thr Ser Tyr Ser Gly Pro Tyr Pro Ala Ala Ala
245          60              65                 70
247 Pro Pro Val Pro Ala Ser Asn Tyr Pro Thr Ile Ser Arg Pro Leu Val
248       75              80                 85
250 Cys Arg Phe Gly Tyr Gln Met Asp Glu Gly Asn Gln Cys Val Asp Val
251 90                95               100                105
253 Asp Glu Cys Ala Thr Asp Ser His Gln Cys Asn Pro Thr Gln Ile Cys
254             110              115               120
256 Ile Asn Thr Glu Gly Gly Tyr Thr Cys Ser Cys Thr Asp Gly Tyr Trp
257             125              130               135
259 Leu Leu Glu Gly Gln Cys Leu Asp Ile Asp Glu Cys Arg Tyr Gly Tyr
260          140              145               150
262 Cys Gln Gln Leu Cys Ala Asn Val Pro Gly Ser Tyr Ser Cys Thr Cys
263       155              160               165
265 Asn Pro Gly Phe Thr Leu Asn Asp Asp Gly Arg Ser Cys Gln Asp Val
266 170              175               180                185
268 Asn Glu Cys Glu Thr Glu Asn Pro Cys Val Gln Thr Cys Val Asn Thr
269              190               195               200
271 Tyr Gly Ser Phe Ile Cys Arg Cys Asp Pro Gly Tyr Glu Leu Glu Glu
272             205              210               215
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[handwritten annotations in right margin:]
(see Error summary sheet)
(see item 10 on Sheet)
insert the MANDATORY numeric identifier whenever <221>, <222> or <223> is shown

RAW SEQUENCE LISTING   DATE: 04/25/2001
PATENT APPLICATION: US/09/674,379   TIME: 07:41:15

Input Set : **A:\es.txt**
Output Set: **N:\CRF3\04252001\I674379.raw**

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274 Asp Gly Ile His Cys Ser Asp Met Asp Glu Cys Ser Phe Ser Glu Phe
275         220             225             230
277 Leu Cys Gln His Glu Cys Val Asn Gln Pro Gly Ser Tyr Phe Cys Ser
278     235             240          .      245
280 Cys Pro Pro Gly Tyr Val Leu Leu Asp Asp Asn Arg Ser Cys Gln Asp
281 250             255             260                 265
283 Ile Asn Glu Cys Glu His Arg Asn His Thr Cys Thr Ser Leu Gln Thr
284             270             275             280
286 Cys Tyr Asn Leu Gln Gly Gly Phe Lys Cys Ile Asp Pro Ile Ser Cys
287         285             290             295
289 Glu Glu Pro Tyr Leu Leu Ile Gly Glu Asn Arg Cys Met Cys Pro Ala
290  ·      300             305             310
292 Glu His Thr Ser Cys Arg Asp Gln Pro Phe Thr Ile Leu Tyr Arg Asp
293     315             320             325
295 Met Asp Val Val Ser Gly Arg Ser Val Pro Ala Asp Ile Phe Gln Met
296 330             335             340                 345
298 Gln Ala Thr Thr Arg Tyr Pro Gly Ala Tyr Tyr Ile Phe Gln Ile Lys
299             350             355             360
301 Ser Gly Asn Glu Gly Arg Glu Phe Tyr Met Arg Gln Thr Gly Pro Ile
302         365             370             375
304 Ser Ala Thr Leu Val Met Thr Arg Pro Ile Lys Gly Pro Arg Asp Ile
305         380             385             390
307 Gln Leu Asp Leu Glu Met Ile Thr Val Asn Thr Val Ile Asn Phe Arg
308     395             400             405
310 Gly Ser Ser Val Ile Arg Leu Arg Ile Tyr Val Ser Gln Tyr Pro Phe
311 410             415             420                 425
315 <210> SEQ ID NO: 4
316 <211> LENGTH: 423
317 <212> TYPE: PRT
318 <213> ORGANISM: Mus musculus
320 <400> SEQUENCE: 4
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322   1           5               10          ·       · 15
324 Asp Ile Asp Glu Cys Arg Thr Ile Pro Glu Ala Cys Arg Gly Asp Met
325             20              25              30
327 Met Cys Val Asn Gln Asn Gly Gly Tyr Leu Cys Ile Pro Arg Thr Asn
328         35              40              45
330 Pro Val Tyr Arg Gly Pro Tyr Ser Asn Pro Tyr Ser Thr Ser Tyr Ser
331     50              55 ·            60
333 Gly Pro Tyr Pro Ala Ala Ala Pro Pro Val Pro Ala Ser Asn Tyr Pro
334 65              70              75                  80
336 Thr Ile Ser Arg Pro Leu Val Cys Arg Phe Gly Tyr Gln Met Asp Glu
337             85              90              95 ˙
339 Gly Asn Gln Cys Val Asp Val Asp Glu Cys Ala Thr Asp Ser His Gln
340             100             105             110
342 Cys Asn Pro Thr Gln Ile Cys Ile Asn Thr Glu Gly Gly Tyr Thr Cys
343         115             120             125     .
345 Ser Cys Thr Asp Gly Tyr Trp Leu Leu Glu Gly Gln Cys Leu Asp Ile
346  ·      130             135             140
```

```
<210> 16
<211> 35
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 16
cgattgaatt ctagacctgc ctcgag(nnnn nnnnn)                          35
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*see
item 10 on
Erva
Summary Sheet*

FYI

          Input Set : **A:\es.txt**
          Output Set: **N:\CRF3\04252001\I674379.raw**

L:10 M:270 C: Current Application Number differs, Replaced Application Number
L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:216 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2
L:637 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:1277 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:16
L:1277 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:16
L:1277 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16